

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 23:44:32 ; Search time 1168.39 Seconds
(without alignments)
471.288 Million cell updates/sec

Title: US-09-913-524-33

Perfect score: 34

Sequence: 1 aggcctcggaggaaacctgctcccatgccaact 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estim:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_estl:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vit:*
 - 22: em_gss_fun:*
 - 23: em_gss_man:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	97.1	251	14	T29423 EST79588 Hu
2	33	97.1	364	10	AW951334 EST363404
C 3	33	97.1	501	9	AI128256 qc33h05.x
C 4	33	97.1	884	13	BI520936 603071335
C 5	33	97.1	899	9	AL568487 AL568487
6	33	97.1	924	9	AL540575 AL540575

ALIGNMENTS

RESULT 1
T29423
LOCUS EST79588 Human Placenta homo sapiens cDNA similar to inhibin, alpha (Hr:1847), mRNA sequence.
DEFINITION T29423
ACCESSION T29423.1 GI:611521
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 251)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,Jr., P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palances,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

C 7	31.4	92.4	599	9	AI220927
C 8	29	85.3	548	14	BQ013783
C 9	26.6	78.2	510	9	AI885743
10	25	73.5	399	12	BE758121
11	25	73.5	464	13	BI849730
12	25	73.5	466	9	AA234854
13	25	73.5	561	12	BE721322
14	25	73.5	1074	13	BM460913
15	25	73.5	1118	13	BM461343
C 16	24	70.6	613	10	AW55078
C 17	24	70.6	641	13	BI186150
18	23.4	68.8	640	12	BC872889
C 19	23.4	68.8	659	13	BI183158
C 20	23.4	68.8	705	13	BI182159
21	23.4	68.8	1172	13	BM461317
C 22	22.6	66.5	582	14	C87829
C 23	22.4	65.9	649	13	BI181741
24	22.4	65.9	978	14	BM804780
C 25	22	64.7	629	13	BM665951
C 26	22	64.7	1521	13	BM563318
27	21.8	64.1	1129	13	BM461356
28	21.2	62.4	845	13	BI857862
C 29	21	61.8	446	9	AA613867
30	20.8	61.2	343	17	B81629
31	20.8	61.2	485	14	BM838500
32	20.8	61.2	539	13	BM127079
33	20.8	61.2	575	17	A2812884
34	20.8	61.2	800	13	BI087023
35	20.8	61.2	927	9	AL532730
36	20.6	60.6	425	14	N41644
C 37	20.6	60.6	716	17	AZ624232
38	20.6	60.6	775	14	BQ571532
C 39	20.4	60.0	503	12	BG625183
C 40	20.4	60.0	669	17	AG148285
41	20.4	60.0	914	14	BQ433546
42	20.4	60.0	976	13	BI770561
C 43	20.4	60.0	1149	14	BM806299
44	20.2	59.4	392	13	BM041782
C 45	20.2	59.4	466	10	AW475765

T29423 251 bp mRNA linear EST 06-SEP-1995
EST79588 Human Placenta homo sapiens cDNA similar to inhibin, alpha (Hr:1847), mRNA sequence.

T29423.1 GI:611521

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,Jr., P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palances,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)

Seq primer: M13 Reverse.

FEATURES location/Qualifiers

source

1..251
/organism="Homo sapiens"
/db_xref="ATCC (inhost):106213"
/db_xref="taxon:9606"
/clone_lib="Human Placenta"
/note="Organ: placenta"

BASE COUNT 47 a 85 c 67 g 51 t 1 others

Query Match 97.1%; Score 33; DB 14; Length 251;

Best Local Similarity 97.1%; Pred. No. 0.074;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 34

|||||

Db 94 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 127

RESULT 2

AW951334

LOCUS

DEFINITION EST363404 MAGE resequenes, MAGB Homo sapiens cDNA, mRNA sequence.

ACCESSION AW951334

VERSION AW951334.1 GI:8141005

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 364)

AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.

Assessment of gene expression patterns in a model of colon tumor

metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org

Plate: 26

Seq primer: Reverse.

FEATURES location/Qualifiers

source

1..364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequenes, MAGB"
/note="Vector: pBluescriptskm"

BASE COUNT 59 a 135 c 96 g 74 t

Query Match

Best Local Similarity 97.1%; Score 33; DB 10; Length 364;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 34

|||||

Db 94 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 127

RESULT 3

AI128256/c

LOCUS

DEFINITION qc33r05.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:1711449 3' similar to gb:M13981 INHIBIN ALPHA CHAIN PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION AI128256

VERSION

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 501)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 832 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 433.

FEATURES

Location/Qualifiers

1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: p7T3-Pac; Site:1: Not I;
Site:2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGAAGATTCGGCCGCTCCCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

BASE COUNT 118 a 117 c 177 g 89 t

ORIGIN

Query Match 97.1%; Score 33; DB 9; Length 501;

Best Local Similarity 97.1%; Pred. No. 0.088;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 34

|||||

Db 445 AGGCTCCGGAGGAACCGCTGCCATGCCCAACT 412

RESULT 4

BI520936/c

LOCUS

DEFINITION 603071335T1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163273 3',
mRNA sequence.

ACCESSION BI520936

VERSION

KEYWORDS EST.

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 884)

AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cygaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1A11405 row: f column: 10
High quality sequence start: 2
High quality sequence stop: 726.
High quality sequence stop: 726.

FEATURES source

1. .884
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5163273"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

BASE COUNT 175 a 231 c 327 g 151 t
ORIGIN

Query Match 97.1%; Score 33; DB 13; Length 884;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 34
|||||
Db 458 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 425

RESULT 5 AL568487/c

LOCUS AL568487 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE002YE07 3 prime
DEFINITION , mRNA sequence.

ACCESSION AL568487
VERSION AL568487.1 GI:12922875

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 899)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES source

1. .899
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YE07"
/clone_lib="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetechn.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 184 a 229 c 318 g 159 t 9 others
ORIGIN

Query Match 97.1%; Score 33; DB 9; Length 899;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 34
|||||
Db 458 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 425

RESULT 6 AL540575

LOCUS AL540575 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE002YE07 5 prime
DEFINITION , mRNA sequence.

ACCESSION AL540575

VERSION AL540575.1 GI:12870853

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES source

1. .924
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YE07"
/clone_lib="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetechn.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT 153 a 307 c 299 g 165 t

ORIGIN

Query Match 97.1%; Score 33; DB 9; Length 924;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 34
|||||
Db 838 AGGCTCCGGAGGAACCGCTGCCATGCCAACT 871

RESULT 7 A1220927/c

LOCUS A1220927 599 bp mRNA linear EST 29-NOV-1998
DEFINITION q908a11.x1 Soares_placenta_8to9weeks_2Nbui8to9W Homo sapiens cDNA

clone IMAGE:1758908 3' similar to gb:M13981 INH1BIN ALPHA CHAIN
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION A1220927
 VERSION A1220927.1 GI:3803130
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 599)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL: contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 761 Std Error: 0.00
 Seq primer: 40UP from Gibco
 High quality sequence stop: 379.

FEATURES

source

1..599
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1758908"

/clone_lib="Soares.placenta.8to9weeks_2NbpP8to9W"
 /dev_stage="two placenta: one from 8 weeks and another
 from 9 weeks post conception"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCGATTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

M.Fatima Bonaldo."

BASE COUNT 135 a 142 c 203 g 115 t 4 others

ORIGIN

Query Match 92.4%; Score 31.4; DB 9; Length 599;

Best Local Similarity 94.1%; Pred. NO. 0.34;

Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGCCTCGGAGAACCGTCGCCATGCCAACT 34

|||||

DB 540 AGGCCTCGGAGAACCGTCGCCATGCCAACT 507

|||||

RESULT 8

BQ013783/C

LOCUS

BQ013783 548 bp mRNA linear EST 26-MAR-2002

DEFINITION

UI-1-BCL1P-alb-q-08-0-UI.s1 NCLCGAP_P13 Homo sapiens cDNA clone

UI-1-BCL1P-alb-q-08-0-UI 3', mRNA sequence.

ACCESSION

BQ013783

VERSION

BQ013783.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 548)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Steven Brown
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 www-bio.llnl.gov/bbrp/image/image.html

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..548

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-1-BCL1P-alb-q-08-0-UI"

/clone_lib="NCI_CGAP_P13"

/tissue_type="Placenta"

/dev_stage="8-9 weeks"

/lab_host="DH10B (L.C. Technologies)"

/note="Organ: Placenta; Vector: pT73-Pac (Pharmacia) with
 a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI_CGAP_P13 is a subcloned cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are GA, AGGA. For
 additional information, contact: Bento Soares,
bento-soares@uiowa.edu
 TAG_L1B-UI-1-BCL1P
 TAG_TISSUE=placenta human 8 week
 TAG_SEQ=GA"

BASE COUNT 122 a 123 c 185 g 118 t

ORIGIN

Query Match 85.3%; Score 29; DB 14; Length 548;

Best Local Similarity 96.7%; Pred. No. 2.3;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTCGGAGGAGAACCGTCGCCATGCCAACT 34

|||||

DB 548 CTCGGAGGAGAACCGTCGCCATGCCAACT 519

|||||

RESULT 9

A1885743/C

LOCUS

A1885743

DEFINITION

w161a07.x1 NCI_CGAP_Bru25 Homo sapiens cDNA clone IMAGE:2429364 3',
 similar to q0-M13981 INH1BIN ALPHA CHAIN PRECURSOR (HUMAN);, mRNA
 sequence.

ACCESSION

A1885743

VERSION

A1885743.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 510)

AUTHORS

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGAP), Tumor Gene Index

JOURNAL

Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

1. .399
/organism="Bos taurus"

Matches	28;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
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Oy 1 AGGCCTCCGAGGACCGNCTGCCCATGCCAC 34
||||||| ||||| || ||||||||| |||
Db 75 AGGCCTCCGAGGAGCGCGCGCCATGCCGACT 108

RESULT 12
AA234854
LOCUS AA234854 466 bp mRNA linear EST 06-AUG-1997
DEFINITION zrf77g01.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:669456 5'
similar to gb:MI3981 INHIBIN ALPHA CHAIN PRECURSOR (HUMAN); mRNA
sequence.
ACCESSION AA234854
VERSION AA234854.1 GI:1859384
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
TITLE Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 676 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Source Location/Qualifiers
1..466
/organism="Homo sapiens"
/db_xref="GDB:563423"
/db_xref="taxon:9606"
/clone="IMAGE:669456"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="Bh10H"
/Note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not 1;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NHMPu, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following BAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 79 a 151 c 119 g 116 t
ORIGIN
Query Match 73.5%; Score 25; DB 9; Length 466;
Best Local Similarity 82.4%; Pred. No. 58;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 AGGCCTCCGAGGACCGNCTGCCCATGCCAACT 34
||||||| ||||| || ||||||||| |||
Db 62 AGGCCTCCGAGGACCGCGCTGCCATGCCAACT 95

RESULT 13
BE721322
LOCUS BE721322 561 bp mRNA linear EST 25-APR-2001
DEFINITION 188456 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE721322
VERSION BE721322.1 GI:10122618
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 561)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
JOURNAL 21180013
MEDLINE
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGGATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 39 row: M column: 6
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Source Location/Qualifiers
1..561
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="Bh10H"
/Note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 80 a 224 c 158 g 99 t
ORIGIN
Query Match 74.5%; Score 25; DB 12; Length 561;
Best Local Similarity 82.4%; Pred. No. 60;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 AGGCCTCCGAGGACCGNCTGCCCATGCCAACT 34
||||||| ||||| || ||||||||| |||
Db 489 AGGCCTCCGAGGAGCGCGCGCCCATGCCGACT 522

RESULT 14
BM460913
LOCUS BM460913 1074 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6419289 NCI_CGAP_Ov44 Mus musculus cDNA clone
IMAGE:3504258 5', mRNA sequence.
ACCESSION BM460913
VERSION BM460913.1 GI:18509953
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1074)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

```

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: ccapsb-re@mail.nih.gov
 Tissue Procurement: Aaron Hsueh
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM12145 row: f column: 03
 High quality sequence start: 16
 High quality sequence stop: 739.
 Location/Qualifiers

FEATURES

source

1. .1074
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5504258"
 /clone_lib="NCI_CGAP_Ov44"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: ovary, PMSG-treated; Vector:
 PCMV-SPORT6.ccdB; Site_1: EcoRV; Site_2: NotI; Cloned
 unidirectionally. Primer: Oligo dt. Average insert size
 2.2 kb. Library constructed by Life Technologies. Note:
 this is a NCI_CGAP Library."

BASE COUNT 176 a 343 c 319 g 232 t 4 others
 ORIGIN

Query Match 73.5%; Score 25; DB 13; Length 1074;

Best Local Similarity 82.4%; Pred. No. 71;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCCCTCCGAGGAAACCGTGGCCATGCCCAACT 34
 ||||| ||||| ||||| ||||| ||||| ||
 Db 815 AGCCCTCCGAGGAAACCGTGGCCATGCCCTTCT 848

RESULT 15

BM461343

LOCUS

DEFINITION BM461343 1118 bp mRNA linear EST 05-FEB-2002
 AGENCOURT_6419744 NCI_CGAP_Ov44 Mus musculus cDNA clone
 IMAGE:5504094 5', mRNA sequence.

ACCESSION BM461343

VERSION BM461343.1 GI:18510383

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 1118)

NIH-MGC <http://mqc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: ccapsb-re@mail.nih.gov

Tissue Procurement: Aaron Hsueh

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM12144 row: o column: 07

High quality sequence stop: 672.

Location/Qualifiers

1. .1118

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:5504094"

/clone_lib="NCI_CGAP_Ov44"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: ovary, PMSG-treated; Vector:
 PCMV-SPORT6.ccdB; Site_1: EcoRV; Site_2: NotI; Cloned
 unidirectionally. Primer: Oligo dt. Average insert size

FEATURES

source

1. .1118
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5504094"
 /clone_lib="NCI_CGAP_Ov44"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: ovary, PMSG-treated; Vector:
 PCMV-SPORT6.ccdB; Site_1: EcoRV; Site_2: NotI; Cloned
 unidirectionally. Primer: Oligo dt. Average insert size

2.2 kb. Library constructed by Life Technologies. Note:
 this is a NCI_CGAP Library."
 BASE COUNT 179 a 372 c 323 g 244 t
 ORIGIN

Query Match 73.5%; Score 25; DB 13; Length 1118;
 Best Local Similarity 82.4%; Pred. No. 72;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCCCTCCGAGGAAACCGTGGCCATGCCCAACT 34
 ||||| ||||| ||||| ||||| ||||| ||
 Db 793 AGCCCTCCGAGGAAACCGTGGCCATGCCCTTCT 826

Search completed: March 11, 2003, 10:26:00
 Job time : 1171.39 secs